1635 1600

ENTERED

Serial Number: 09/700,906 B

CRF Processing Date: 11/21/2002
Edited by:
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line. # 15

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

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DEC 04 2002
TECH CENTER 1600/2900

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

1600

RAW SEQUENCE LISTING   DATE: 11/21/2002
PATENT APPLICATION: US/09/700,906B   TIME: 10:13:50

Input Set : **A:\US Serial 09-700906-Sequence-List-11-06-02.txt**
Output Set: **N:\CRF4\11212002\I700906B.raw**

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 4 <110> APPLICANT: Faustus Forschungs Cie. Translational Cancer Research GmbH
 6 <120> TITLE OF INVENTION: Antisense oligonucleotides for treating proliferating cells
 8 <130> FILE REFERENCE: PA32470US-01938
10 <140> CURRENT APPLICATION NUMBER: US/09/700,906B
11 <141> CURRENT FILING DATE: 2001-02-26
13 <150> PRIOR APPLICATION NUMBER: DE 198 22 954.2
14 <151> PRIOR FILING DATE: 1998-05-22
16 <160> NUMBER OF SEQ ID NOS: 5
18 <170> SOFTWARE: PatentIn Vers. 2.0
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ERRORED SEQUENCES

Does Not Comply
Corrected Diskette Needed

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1582 <210> SEQ ID NO: 5
1583 <211> LENGTH: 25
1584 <212> TYPE: DNA
1585 <213> ORGANISM: Artificial sequence
1587 <220> FEATURE:
1588 <223> OTHER INFORMATION: Description of the artificial sequence: missense
1589         Synthetic oligonucleotide
1591 <400> SEQUENCE: 5
1592 agtactcagt aacgcctacg gtaag                                    25
E--> 1594  -42-  delete
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VERIFICATION SUMMARY   DATE: 11/21/2002
PATENT APPLICATION: **US/09/700,906B**   TIME: 10:13:51

Input Set : **A:\US Serial 09-700906-Sequence-List-11-06-02.txt**
Output Set: **N:\CRF4\11212002\I700906B.raw**

L:1594 M:254 E: No. of Bases conflict, this line has no nucleotides.

1600

RAW SEQUENCE LISTING   DATE: 11/27/2002
PATENT APPLICATION: US/09/700,906B   TIME: 18:13:46

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\11272002\I700906B.raw

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 4 <110> APPLICANT: Faustus Forschungs Cie. Translational Cancer Research GmbH
 6 <120> TITLE OF INVENTION: Antisense oligonucleotides for treating proliferating cells
 8 <130> FILE REFERENCE: PA32470US-01938
10 <140> CURRENT APPLICATION NUMBER: US/09/700,906B
11 <141> CURRENT FILING DATE: 2001-02-26
13 <150> PRIOR APPLICATION NUMBER: DE 198 22 954.2
14 <151> PRIOR FILING DATE: 1998-05-22
16 <160> NUMBER OF SEQ ID NOS: 5
18 <170> SOFTWARE: PatentIn Vers. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 12493
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (197)..(9964)
29 <400> SEQUENCE: 1
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32 gacgagcggt ggttcgacaa gtggccttgc gggccggatc gtcccagtgg aagagttgta 120
34 aatttgcttc tggccttccc ctacggatta tacctggcct tcccctacgg attatactca 180
36 acttactgtt tagaaa atg tgg ccc acg aga cgc ctg gtt act atc aaa agg 232
37                    Met Trp Pro Thr Arg Arg Leu Val Thr Ile Lys Arg
38                     1               5                  10
40 agc ggg gtc gac ggt ccc cac ttt ccc ctg agc ctc agc acc tgc ttg  280
41 Ser Gly Val Asp Gly Pro His Phe Pro Leu Ser Leu Ser Thr Cys Leu
42          15               20                  25
44 ttt gga agg ggt att gaa tgt gac atc cgt atc cag ctt cct gtt gtg  328
45 Phe Gly Arg Gly Ile Glu Cys Asp Ile Arg Ile Gln Leu Pro Val Val
46      30               35                  40
48 tca aaa caa cat tgc aaa gtt gaa atc cat gag cag gag gca ata tta  376
49 Ser Lys Gln His Cys Lys Val Glu Ile His Glu Gln Glu Ala Ile Leu
50  45               50                  55                  60
52 cat aat ttc agt tcc aca aat cca aca caa gta aat ggg tct gtt att  424
53 His Asn Phe Ser Ser Thr Asn Pro Thr Gln Val Asn Gly Ser Val Ile
54              65                  70                  75
56 gat gag cct gta cgg cta aaa cat gga gat gta ata act att att gat  472
57 Asp Glu Pro Val Arg Leu Lys His Gly Asp Val Ile Thr Ile Ile Asp
58          80                  85                  90
60 cgt tcc ttc agg tat gaa aat gaa agt ctt cag aat gga agg aag tca  520
61 Arg Ser Phe Arg Tyr Glu Asn Glu Ser Leu Gln Asn Gly Arg Lys Ser
62          95                  100                 105
64 act gaa ttt cca aga aaa ata cgt gaa cag gag cca gca cgt cgt gtc  568
65 Thr Glu Phe Pro Arg Lys Ile Arg Glu Gln Glu Pro Ala Arg Arg Val
```

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66    110                    115                    120
68 tca aga tct agc ttc tct tct gac cct gat gag aaa gct caa gat tcc    616
69 Ser Arg Ser Ser Phe Ser Ser Asp Pro Asp Glu Lys Ala Gln Asp Ser
70 125                    130                    135                    140
72 aag gcc tat tca aaa atc act gaa gga aaa gtt tca gga aat cct cag    664
73 Lys Ala Tyr Ser Lys Ile Thr Glu Gly Lys Val Ser Gly Asn Pro Gln
74                    145                    150                    155
76 gta cat atc aag aat gtc aaa gaa gac agt acc gca gat gac tca aaa    712
77 Val His Ile Lys Asn Val Lys Glu Asp Ser Thr Ala Asp Asp Ser Lys
78                    160                    165                    170
80 gac agt gtt gct cag gga aca act aat gtt cat tcc tca gaa cat gct    760
81 Asp Ser Val Ala Gln Gly Thr Thr Asn Val His Ser Ser Glu His Ala
82         175                    180                    185
84 gga cgt aat ggc aga aat gca gct gat ccc att tct ggg gat ttt aaa    808
85 Gly Arg Asn Gly Arg Asn Ala Ala Asp Pro Ile Ser Gly Asp Phe Lys
86    190                    195                    200
88 gaa att tcc agc gtt aaa tta gtg agc cgt tat gga gaa ttg aag tct    856
89 Glu Ile Ser Ser Val Lys Leu Val Ser Arg Tyr Gly Glu Leu Lys Ser
90 205                    210                    215                    220
92 gtt ccc act aca caa tgt ctt gac aat agc aaa aaa aat gaa tct ccc    904
93 Val Pro Thr Thr Gln Cys Leu Asp Asn Ser Lys Lys Asn Glu Ser Pro
94                    225                    230                    235
96 ttt tgg aag ctt tat gag tca gtg aag aaa gag ttg gat gta aaa tca    952
97 Phe Trp Lys Leu Tyr Glu Ser Val Lys Lys Glu Leu Asp Val Lys Ser
98                    240                    245                    250
100 caa aaa gaa aat gtc cta cag tat tgt aga aaa tct gga tta caa act    1000
101 Gln Lys Glu Asn Val Leu Gln Tyr Cys Arg Lys Ser Gly Leu Gln Thr
102         255                    260                    265
104 gat tac gca aca gag aaa gaa agt gct gat ggt tta cag ggg gag acc    1048
105 Asp Tyr Ala Thr Glu Lys Glu Ser Ala Asp Gly Leu Gln Gly Glu Thr
106    270                    275                    280
108 caa ctg ttg gtc tcg cgt aag tca aga cca aaa tct ggt ggg agc ggc    1096
109 Gln Leu Leu Val Ser Arg Lys Ser Arg Pro Lys Ser Gly Gly Ser Gly
110 285                    290                    295                    300
112 cac gct gtg gca gag cct gct tca cct gaa caa gag ctt gac cag aac    1144
113 His Ala Val Ala Glu Pro Ala Ser Pro Glu Gln Glu Leu Asp Gln Asn
114                    305                    310                    315
116 aag ggg aag gga aga gac gtg gag tct gtt cag act ccc agc aag gct    1192
117 Lys Gly Lys Gly Arg Asp Val Glu Ser Val Gln Thr Pro Ser Lys Ala
118                    320                    325                    330
120 gtg ggc gcc agc ttt cct ctc tat gag ccg gct aaa atg aag acc cct    1240
121 Val Gly Ala Ser Phe Pro Leu Tyr Glu Pro Ala Lys Met Lys Thr Pro
122         335                    340                    345
124 gta caa tat tca cag caa caa aat tct cca caa aaa cat aag aac aaa    1288
125 Val Gln Tyr Ser Gln Gln Gln Asn Ser Pro Gln Lys His Lys Asn Lys
126    350                    355                    360
128 gac ctg tat act act ggt aga aga gaa tct gtg aat ctg ggt aaa agt    1336
129 Asp Leu Tyr Thr Thr Gly Arg Arg Glu Ser Val Asn Leu Gly Lys Ser
130 365                    370                    375                    380
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132 gaa ggc ttc aag gct ggt gat aaa act ctt act ccc agg aag ctt tca    1384
133 Glu Gly Phe Lys Ala Gly Asp Lys Thr Leu Thr Pro Arg Lys Leu Ser
134             385             390             395
136 act aga aat cga aca cca gct aaa gtt gaa gat gca gct gac tct gcc    1432
137 Thr Arg Asn Arg Thr Pro Ala Lys Val Glu Asp Ala Ala Asp Ser Ala
138             400             405             410
140 act aag cca gaa aat ctc tct tcc aaa acc aga gga agt att cct aca    1480
141 Thr Lys Pro Glu Asn Leu Ser Ser Lys Thr Arg Gly Ser Ile Pro Thr
142             415             420             425
144 gat gtg gaa gtt ctg cct acg gaa act gaa att cac aat gag cca ttt    1528
145 Asp Val Glu Val Leu Pro Thr Glu Thr Glu Ile His Asn Glu Pro Phe
146     430             435             440
148 tta act ctg tgg ctc act caa gtt gag agg aag atc caa aag gat tcc    1576
149 Leu Thr Leu Trp Leu Thr Gln Val Glu Arg Lys Ile Gln Lys Asp Ser
150 445             450             455             460
152 ctc agc aag cct gag aaa ttg ggc act aca gct gga cag atg tgc tct    1624
153 Leu Ser Lys Pro Glu Lys Leu Gly Thr Thr Ala Gly Gln Met Cys Ser
154             465             470             475
156 ggg tta cct ggt ctt agt tca gtt gat atc aac aac ttt ggt gat tcc    1672
157 Gly Leu Pro Gly Leu Ser Ser Val Asp Ile Asn Asn Phe Gly Asp Ser
158             480             485             490
160 att aat gag agt gag gga ata cct ttg aaa aga agg cgt gtg tcc ttt    1720
161 Ile Asn Glu Ser Glu Gly Ile Pro Leu Lys Arg Arg Arg Val Ser Phe
162             495             500             505
164 ggt ggg cac cta aga cct gaa cta ttt gat gaa aac ttg cct cct aat    1768
165 Gly Gly His Leu Arg Pro Glu Leu Phe Asp Glu Asn Leu Pro Pro Asn
166     510             515             520
168 acg cct ctc aaa agg gga gaa gcc cca acc aaa aga aag tct ctg gta    1816
169 Thr Pro Leu Lys Arg Gly Glu Ala Pro Thr Lys Arg Lys Ser Leu Val
170 525             530             535             540
172 atg cac act cca cct gtc ctg aag aaa atc atc aag gaa cag cct caa    1864
173 Met His Thr Pro Pro Val Leu Lys Lys Ile Ile Lys Glu Gln Pro Gln
174             545             550             555
176 cca tca gga aaa caa gag tca ggt tca gaa atc cat gtg gaa gtg aag    1912
177 Pro Ser Gly Lys Gln Glu Ser Gly Ser Glu Ile His Val Glu Val Lys
178             560             565             570
180 gca caa agc ttg gtt ata agc cct cca gct cct agt cct agg aaa act    1960
181 Ala Gln Ser Leu Val Ile Ser Pro Pro Ala Pro Ser Pro Arg Lys Thr
182             575             580             585
184 cca gtt gcc agt gat caa cgc cgt agg tcc tgc aaa aca gcc cct gct    2008
185 Pro Val Ala Ser Asp Gln Arg Arg Arg Ser Cys Lys Thr Ala Pro Ala
186     590             595             600
188 tcc agc agc aaa tct cag aca gag gtt cct aag aga gga gga gaa aga    2056
189 Ser Ser Ser Lys Ser Gln Thr Glu Val Pro Lys Arg Gly Gly Glu Arg
190 605             610             615             620
192 gtg gca acc tgc ctt caa aag aga gtg tct atc agc cga agt caa cat    2104
193 Val Ala Thr Cys Leu Gln Lys Arg Val Ser Ile Ser Arg Ser Gln His
194             625             630             635
196 gat att tta cag atg ata tgt tcc aaa aga aga agt ggt gct tcg gaa    2152
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197 Asp Ile Leu Gln Met Ile Cys Ser Lys Arg Arg Ser Gly Ala Ser Glu
198             640             645             650
200 gca aat ctg att gtt gca aaa tca tgg gca gat gta gta aaa ctt ggt    2200
201 Ala Asn Leu Ile Val Ala Lys Ser Trp Ala Asp Val Val Lys Leu Gly
202         655             660             665
204 gca aaa caa aca caa act aaa gtc ata aaa cat ggt cct caa agg tca    2248
205 Ala Lys Gln Thr Gln Thr Lys Val Ile Lys His Gly Pro Gln Arg Ser
206     670             675             680
208 atg aac aaa agg caa aga aga cct gct act cca aag aag cct gtg ggc    2296
209 Met Asn Lys Arg Gln Arg Arg Pro Ala Thr Pro Lys Lys Pro Val Gly
210 685             690             695             700
212 gaa gtt cac agt caa ttt agt aca ggc cac gca aac tct cct tgt acc    2344
213 Glu Val His Ser Gln Phe Ser Thr Gly His Ala Asn Ser Pro Cys Thr
214             705             710             715
216 ata ata ata ggg aaa gct cat act gaa aaa gta cat gtg cct gct cga    2392
217 Ile Ile Ile Gly Lys Ala His Thr Glu Lys Val His Val Pro Ala Arg
218             720             725             730
220 ccc tac aga gtg ctc aac aac ttc att tcc aac caa aaa atg gac ttt    2440
221 Pro Tyr Arg Val Leu Asn Asn Phe Ile Ser Asn Gln Lys Met Asp Phe
222         735             740             745
224 aag gaa gat ctt tca gga ata gct gaa atg ttc aag acc cca gtg aag    2488
225 Lys Glu Asp Leu Ser Gly Ile Ala Glu Met Phe Lys Thr Pro Val Lys
226     750             755             760
228 gag caa ccg cag ttg aca agc aca tgt cac atc gct att tca aat tca    2536
229 Glu Gln Pro Gln Leu Thr Ser Thr Cys His Ile Ala Ile Ser Asn Ser
230 765             770             775             780
232 gag aat ttg ctt gga aaa cag ttt caa gga act gat tca gga gaa gaa    2584
233 Glu Asn Leu Leu Gly Lys Gln Phe Gln Gly Thr Asp Ser Gly Glu Glu
234             785             790             795
236 cct ctg ctc ccc acc tca gag agt ttt gga gga aat gtg ttc ttc agt    2632
237 Pro Leu Leu Pro Thr Ser Glu Ser Phe Gly Gly Asn Val Phe Phe Ser
238             800             805             810
240 gca cag aat gca gca aaa cag cca tct gat aaa tgc tct gca agc cct    2680
241 Ala Gln Asn Ala Ala Lys Gln Pro Ser Asp Lys Cys Ser Ala Ser Pro
242         815             820             825
244 ccc tta aga cgg cag tgt att aga gaa aat gga aac gta gca aaa acg    2728
245 Pro Leu Arg Arg Gln Cys Ile Arg Glu Asn Gly Asn Val Ala Lys Thr
246     830             835             840
248 ccc agg aac acc tac aaa atg act tct ctg gag aca aaa act tca gat    2776
249 Pro Arg Asn Thr Tyr Lys Met Thr Ser Leu Glu Thr Lys Thr Ser Asp
250 845             850             855             860
252 act gag aca gag cct tca aaa aca gta tcc act gta aac agg tca gga    2824
253 Thr Glu Thr Glu Pro Ser Lys Thr Val Ser Thr Val Asn Arg Ser Gly
254             865             870             875
256 agg tct aca gag ttc agg aat ata cag aag cta cct gtg gaa agt aag    2872
257 Arg Ser Thr Glu Phe Arg Asn Ile Gln Lys Leu Pro Val Glu Ser Lys
258             880             885             890
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261 Ser Glu Glu Thr Asn Thr Glu Ile Val Glu Cys Ile Leu Lys Arg Gly
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262        895                    900              905
264 cag aag gca aca cta cta caa caa agg aga gaa gga gag atg aag gaa   2968
265 Gln Lys Ala Thr Leu Leu Gln Gln Arg Arg Glu Gly Glu Met Lys Glu
266        910                    915                920
268 ata gaa aga cct ttt gag aca tat aag gaa aat att gaa tta aaa gaa   3016
269 Ile Glu Arg Pro Phe Glu Thr Tyr Lys Glu Asn Ile Glu Leu Lys Glu
270 925                    930                935                940
272 aac gat gaa aag atg aaa gca atg aag aga tca aga act tgg ggg cag   3064
273 Asn Asp Glu Lys Met Lys Ala Met Lys Arg Ser Arg Thr Trp Gly Gln
274             945                    950                955
276 aaa tgt gca cca atg tct gac ctg aca gac ctc aag agc ttg cct gat   3112
277 Lys Cys Ala Pro Met Ser Asp Leu Thr Asp Leu Lys Ser Leu Pro Asp
278             960                    965                970
280 aca gaa ctc atg aaa gac acg gca cgt ggc cag aat ctc ctc caa acc   3160
281 Thr Glu Leu Met Lys Asp Thr Ala Arg Gly Gln Asn Leu Leu Gln Thr
282        975                    980                985
284 caa gat cat gcc aag gca cca aag agt gag aaa ggc aaa atc act aaa   3208
285 Gln Asp His Ala Lys Ala Pro Lys Ser Glu Lys Gly Lys Ile Thr Lys
286        990                    995                1000
288 atg ccc tgc cag tca tta caa cca gaa cca ata aac acc cca aca cac   3256
289 Met Pro Cys Gln Ser Leu Gln Pro Glu Pro Ile Asn Thr Pro Thr His
290 1005                   1010               1015               1020
292 aca aaa caa cag ttg aag gca tcc ctg ggg aaa gta ggt gtg aaa gaa   3304
293 Thr Lys Gln Gln Leu Lys Ala Ser Leu Gly Lys Val Gly Val Lys Glu
294             1025               1030               1035
296 gag ctc cta gca gtc ggc aag ttc aca cgg acg tca ggg gag acc acg   3352
297 Glu Leu Leu Ala Val Gly Lys Phe Thr Arg Thr Ser Gly Glu Thr Thr
298             1040               1045               1050
300 cac acg cac aga gag cca gca gga gat ggc aag agc atc aga acg ttt   3400
301 His Thr His Arg Glu Pro Ala Gly Asp Gly Lys Ser Ile Arg Thr Phe
302        1055               1060               1065
304 aag gag tct cca aag cag atc ctg gac cca gca gcc cgt gta act gga   3448
305 Lys Glu Ser Pro Lys Gln Ile Leu Asp Pro Ala Ala Arg Val Thr Gly
306    1070               1075               1080
308 atg aag aag tgg cca aga acg cct aag gaa gag gcc cag tca cta gaa   3496
309 Met Lys Lys Trp Pro Arg Thr Pro Lys Glu Glu Ala Gln Ser Leu Glu
310 1085               1090               1095               1100
312 gac ctg gct ggc ttc aaa gag ctc ttc cag aca cca ggt ccc tct gag   3544
313 Asp Leu Ala Gly Phe Lys Glu Leu Phe Gln Thr Pro Gly Pro Ser Glu
314             1105               1110               1115
316 gaa tca atg act gat gag aaa act acc aaa ata gcc tgc aaa tct cca   3592
317 Glu Ser Met Thr Asp Glu Lys Thr Thr Lys Ile Ala Cys Lys Ser Pro
318             1120               1125               1130
320 cca cca gaa tca gtg gac act cca aca agc aca aag caa tgg cct aag   3640
321 Pro Pro Glu Ser Val Asp Thr Pro Thr Ser Thr Lys Gln Trp Pro Lys
322        1135               1140               1145
324 aga agt ctc agg aaa gca gat gta gag gaa gaa ttc tta gca ctc agg   3688
325 Arg Ser Leu Arg Lys Ala Asp Val Glu Glu Glu Phe Leu Ala Leu Arg
326    1150               1155               1160
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VERIFICATION SUMMARY   DATE: 11/27/2002
PATENT APPLICATION: **US/09/700,906B**   TIME: 18:13:47

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\11272002\I700906B.raw**